STN Search Summary

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=> d his

     FILE 'CAPLUS' ENTERED AT 18:12:08 ON 28 JUN 2004
L1          2016 S ML-236 OR PRAVASTATIN
L2           130 S L1 AND GENE
L3             9 S L2 AND PENICILLIUM

L3   ANSWER 1 OF 9  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2003:315995  CAPLUS
TI   Decreasing production cost for mevalotin, an antilipemic agent. One
     transcription factor which improves fermentation productivity for
     pravastatin precursor ML236B
AU   Abe, Yuki
SO   Kagaku to Seibutsu (2003), 41(4), 214-216
DT   Journal; General Review
LA   Japanese

L3   ANSWER 2 OF 9  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2003:305611  CAPLUS
TI   DNA sequence of gene cluster from Penicillium citrinum
     and its use for preparation of pravastatin precursor ML-236B
IN   Abe, Yuki
SO   Jpn. Kokai Tokkyo Koho, 142 pp.
LA   Japanese
     PATENT NO.         KIND  DATE          APPLICATION NO.  DATE
     ---------------    ----  --------      ---------------  --------
PI   JP 2003116567       A2   20030422      JP 2001-316578   20011015
PRAI JP 2001-316578           20011015

L3   ANSWER 3 OF 9  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2002:369763  CAPLUS
TI   Biosynthesis and biotechnological production of statins by filamentous
     fungi and application of these cholesterol-lowering drugs
AU   Manzoni, M.; Rollini, M.
SO   Applied Microbiology and Biotechnology (2002), 58(5), 555-564

L3   ANSWER 4 OF 9  CAPLUS  COPYRIGHT 2004 ACS on STN
AN   2002:240926  CAPLUS
TI   Modulation of secondary metabolite production in fungi by genetic
     engineering for expression of zinc binuclear cluster proteins
IN   Holtzman, Douglas; Madden, Kevin; Maxon, Mary; Sherman, Amir
SO   PCT Int. Appl., 49 pp.
     PATENT NO.         KIND  DATE          APPLICATION NO.  DATE
     ---------------    ----  --------      ---------------  --------
PI   WO 2002024865       A2   20020328      WO 2001-US29288  20010919
     WO 2002024865       A3   20040226
     EP 1409530          A2   20040421      EP 2001-971200   20010919
     US 2004077039       A1   20040422      US 2002-149310   20020610
PRAI US 2000-233564P     P    20000919
     WO 2001-US29288     W    20010919
```

L3 ANSWER 5 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:796334 CAPLUS
TI Genes related to biosynthesis of ML-236B
IN Yoshikawa, Hiroji; Abe, Yuki; Ono, Chiho
SO Eur. Pat. Appl., 146 pp.

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1149919	A2	20011031	EP 2001-303527	20010418
	EP 1149919	A3	20020206		
	CA 2342397	AA	20011018	CA 2001-2342397	20010417
	NO 2001001890	A	20011019	NO 2001-1890	20010417
	ZA 2001003121	A	20011022	ZA 2001-3121	20010417
	US 2003078395	A1	20030424	US 2001-836705	20010417
	BR 2001001518	A	20011113	BR 2001-1518	20010418
	CN 1325959	A	20011212	CN 2001-119655	20010418
	JP 2002315579	A2	20021029	JP 2001-119385	20010418
	NZ 511166	A	20021126	NZ 2001-511166	20010418
PRAI	JP 2000-116591	A	20000418		
	JP 2000-117458	A	20000419		

L3 ANSWER 6 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:300748 CAPLUS
TI Methods for improving secondary metabolite production in fungi
IN Busby, Robert; Doten, Reed; Cali, Brian; Hecht, Peter; Holtzman, Doug; Madden, Kevin; Maxon, Mary; Milne, Todd; Norman, Thea; Royer, John; Salama, Sofie; Sherman, Amir; Silva, Jeff; Summers, Eric; Zhang, Lixin; Mayorga, Maria; Feibelman, Toby
SO PCT Int. Appl., 139 pp.

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001029073	A1	20010426	WO 2000-US28903	20001018
	EP 1237914	A1	20020911	EP 2000-973665	20001018
	JP 2003512039	T2	20030402	JP 2001-531871	20001018
	US 2002128250	A1	20020912	US 2001-801368	20010307
PRAI	US 1999-160587P	P	19991020		
	US 2000-487558	A	20000119		
	WO 2000-US28903	W	20001018		

L3 ANSWER 7 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:137378 CAPLUS
TI Penicillium citrinum genes associated with biosynthesis of ML-236B, precursor of a 3-hydroxy-3-methylglutaryl CoA reductase inhibitor
IN Abe, Yuki; Hosobuchi, Masahiko; Yoshikawa, Hiroji
LA Japanese

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001012814	A1	20010222	WO 2000-JP5420	20000811
	JP 2001112487	A2	20010424	JP 2000-240722	20000809
PRAI	JP 1999-227696	A	19990811		

L3 ANSWER 8 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1999:166732 CAPLUS
TI Manufacture of pravastatin from compactin with transgenic microorganisms expressing a foreign hydroxylase gene
IN Ykema, Adriaantje; Streekstra, Hugo; Luiten, Rudolf Gijsbertus Marie

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9910499	A1	19990304	WO 1998-EP5362	19980824
	AU 9892645	A1	19990316	AU 1998-92645	19980824
	EP 1015600	A1	20000705	EP 1998-945280	19980824
PRAI	EP 1997-306462	A	19970822		
	WO 1998-EP5362	W	19980824		

L3 ANSWER 9 OF 9 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1997:457023 CAPLUS
TI Streptomyces carbophilus cytochrome P 450 gene promoter sequence, use in protein production by fermentation, and use such as for ML-236B hydroxylation and pravastatin sodium production
IN Nobufusa, Serizawa; Ichiro, Watanabe

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 776974	A2	19970604	EP 1996-308648	19961129
	EP 776974	A3	19971008		
	EP 776974	B1	20030502		
	ZA 9609974	A	19970617	ZA 1996-9974	19961127
	US 5830695	A	19981103	US 1996-756592	19961127
	CZ 291991	B6	20030716	CZ 1996-3480	19961127
	CA 2191503	AA	19970530	CA 1996-2191503	19961128
	NO 9605072	A	19970530	NO 1996-5072	19961128
	AU 9674023	A1	19970605	AU 1996-74023	19961128
	AU 715626	B2	20000203		
	JP 09206085	A2	19970812	JP 1996-317745	19961128
	JP 3526708	B2	20040517		
	RU 2140984	C1	19991110	RU 1996-122565	19961128
	CN 1158897	A	19970910	CN 1996-121493	19961129
	AT 239086	E	20030515	AT 1996-308648	19961129
	PT 776974	T	20030829	PT 1996-308648	19961129
	ES 2197938	T3	20040116	ES 1996-308648	19961129
	HK 1004490	A1	20030919	HK 1998-103113	19980415
PRAI	JP 1995-310247	A	19951129		

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2004, 22:47:36 ; Search time 8769 Seconds
(without alignments)
6821.004 Million cell updates/sec

Title: US-09-836-705-41
Perfect score: 1380
Sequence: 1 atgtccctgccgcatgcaac.....agaaacacaatattgcttag 1380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Applicants'

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	1380	100.0	1380	6	BD178141 JP2002315579	BD178141 On the st
c	2	1222	88.6	34203	6	BD013765 JP2001112487	BD013765 ML-236B b
	3	1222	88.6	34203	6	BD013766 "	BD013766 ML-236B b
c	4	1222	88.6	34203	6	BD093553 WO 01/12814	BD093553 DNAs rela
	5	1222	88.6	34203	6	BD093554 "	BD093554 DNAs rela
c	6	1222	88.6	34203	6	BD178102	BD178102 On the st
	7	1222	88.6	34203	6	BD178103	BD178103 On the st
c	8	1222	88.6	38231	8	AB072893 GenBank 10/8/02	AB072893 Penicilli
c	9	511.4	37.1	562	6	BD013798	BD013798 ML-236B b
c	10	511.4	37.1	562	6	BD093586	BD093586 DNAs rela
c	11	511.4	37.1	562	6	BD178135	BD178135 On the st
	12	472.4	34.2	541	6	BD013786	BD013786 ML-236B b
	13	472.4	34.2	541	6	BD093574	BD093574 DNAs rela
	14	472.4	34.2	541	6	BD178123	BD178123 On the st
	15	182.8	13.2	1407	6	AX684834	AX684834 Sequence
	16	128.6	9.3	1509	6	AX684832	AX684832 Sequence
	17	128.6	9.3	43328	8	ATLOVBSGC2	AF141925 Aspergill
	18	49.8	3.6	2000	6	AX655393	AX655393 Sequence
c	19	43.4	3.1	1246	6	AX164174	AX164174 Sequence
	20	43.2	3.1	255678	2	AC099432	AC099432 Rattus no
c	21	43	3.1	245711	2	AC098021	AC098021 Rattus no
	22	43	3.1	253401	2	AC097127	AC097127 Rattus no
c	23	42	3.0	2000	6	AX655393	AX655393 Sequence
c	24	41.8	3.0	125026	10	AC091616	AC091616 Rattus no
	25	41.8	3.0	241327	2	AC127126	AC127126 Rattus no
	26	41.8	3.0	251075	2	AC132995	AC132995 Rattus no
c	27	41.8	3.0	282995	2	AC131530	AC131530 Rattus no
	28	41.6	3.0	242082	2	AC121699	AC121699 Rattus no
	29	41.6	3.0	268930	2	AC119562	AC119562 Rattus no
	30	41.4	3.0	172307	9	AL590609	AL590609 Human DNA
c	31	40.4	2.9	169071	9	AC092888	AC092888 Homo sapi
c	32	40.4	2.9	196962	9	AC090017	AC090017 Homo sapi
c	33	40.2	2.9	98378	8	AP004845	AP004845 Oryza sat

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OM nucleic - nucleic search, using sw model

Run on: June 3, 2004, 22:45:01 ; Search time 829 Seconds
(without alignments)
7071.789 Million cell updates/sec

Title: US-09-836-705-41
Perfect score: 1380
Sequence: 1 atgtccctgccgcatgcaac.....agaaacacaatattgcttag 1380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	1380	100.0	1380	6	AAS16808	Aas16808 Penicilli
	2	1377	99.8	1377	9	ADE81190	Ade81190 MlcR codi
c	3	1222	88.6	34203	4	AAF74546	Aaf74546 Penicilli
c	4	1222	88.6	34203	6	AAS16770	Aas16770 Penicilli
	5	1222	88.6	34263	4	AAF74547	Aaf74547 Penicilli
c	6	1222	88.6	72149	9	ADE81173	Ade81173 ML-236B s
c	7	511.4	37.1	562	4	AAF74579	Aaf74579 ML-236B b
c	8	511.4	37.1	562	6	AAS16802	Aas16802 Penicilli

EP 119 919 PD: 10/31/01
JP 2003 116567
WO 01/12814

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 3, 2004, 20:04:03 ; Search time 131 Seconds
(without alignments)
5846.048 Million cell updates/sec

Title: US-09-836-705-41
Perfect score: 1380
Sequence: 1 atgtccctgccgcatgcaac.....agaaacacaatattgcttag 1380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	128.6	9.3	1512	4	US-09-215-694-27	Sequence 27, Appl
	2	128.6	9.3	33000	4	US-09-215-694-18	Sequence 18, Appl
	3	35.6	2.6	832	4	US-09-621-976-2813	Sequence 2813, Ap
	4	35.4	2.6	3302	4	US-09-620-312D-475	Sequence 475, App
c	5	34.6	2.5	1127	4	US-09-976-594-1102	Sequence 1102, Ap
c	6	34.4	2.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	7	34.4	2.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	8	33.2	2.4	90541	4	US-09-759-359A-3	Sequence 3, Appli
	9	32.6	2.4	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	10	32.2	2.3	290	4	US-09-313-294A-6837	Sequence 6837, Ap
	11	32.2	2.3	1218	4	US-09-336-536-22	Sequence 22, Appl
	12	32.2	2.3	1721	4	US-09-336-536-21	Sequence 21, Appl

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OM nucleic - nucleic search, using sw model

Run on: June 3, 2004, 21:48:02 ; Search time 863 Seconds
(without alignments)
7294.965 Million cell updates/sec

Title: US-09-836-705-41
Perfect score: 1380
Sequence: 1 atgtccctgccgcatgcaac.....agaaacacaatattgcttag 1380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	1380	100.0	1380	10	US-09-836-705-41	Sequence 41, Appl
c	2	1222	88.6	34203	10	US-09-836-705-1	Sequence 1, Appli
	3	1222	88.6	34203	10	US-09-836-705-2	Sequence 2, Appli
c	4	511.4	37.1	562	10	US-09-836-705-34	Sequence 34, Appl
	5	472.4	34.2	541	10	US-09-836-705-22	Sequence 22, Appl
	6	187.2	13.6	1410	10	US-09-974-760B-81	Sequence 81, Appl
	7	185.6	13.4	1410	10	US-09-974-760B-69	Sequence 69, Appl
	8	185.6	13.4	1410	10	US-09-974-760B-73	Sequence 73, Appl
	9	184.4	13.4	1410	10	US-09-974-760B-70	Sequence 70, Appl
	10	184.4	13.4	1410	10	US-09-974-760B-74	Sequence 74, Appl
	11	184.4	13.4	1410	10	US-09-974-760B-80	Sequence 80, Appl
	12	184	13.3	1410	10	US-09-974-760B-85	Sequence 85, Appl
	13	182.8	13.2	1407	17	US-10-149-310-153	Sequence 153, App
	14	182.8	13.2	1410	9	US-09-801-368-181	Sequence 181, App
	15	182.8	13.2	1410	10	US-09-974-760B-72	Sequence 72, Appl
	16	182.8	13.2	1410	10	US-09-974-760B-76	Sequence 76, Appl
	17	182.8	13.2	1410	10	US-09-974-760B-78	Sequence 78, Appl
	18	182.8	13.2	1410	10	US-09-974-760B-82	Sequence 82, Appl
	19	182.8	13.2	1410	10	US-09-974-760B-84	Sequence 84, Appl
	20	182.8	13.2	1410	10	US-09-974-760B-92	Sequence 92, Appl
	21	181.2	13.1	1410	10	US-09-974-760B-68	Sequence 68, Appl
	22	181.2	13.1	1410	10	US-09-974-760B-77	Sequence 77, Appl
	23	181.2	13.1	1410	10	US-09-974-760B-83	Sequence 83, Appl
	24	181.2	13.1	1410	10	US-09-974-760B-89	Sequence 89, Appl
	25	180.8	13.1	1410	10	US-09-974-760B-71	Sequence 71, Appl
	26	180.8	13.1	1410	10	US-09-974-760B-79	Sequence 79, Appl
	27	180.8	13.1	1410	10	US-09-974-760B-88	Sequence 88, Appl
	28	179.6	13.0	1410	10	US-09-974-760B-67	Sequence 67, Appl
	29	179.6	13.0	1410	10	US-09-974-760B-75	Sequence 75, Appl
	30	179.6	13.0	1410	10	US-09-974-760B-90	Sequence 90, Appl
	31	178	12.9	1410	10	US-09-974-760B-66	Sequence 66, Appl
	32	178	12.9	1410	10	US-09-974-760B-86	Sequence 86, Appl
	33	177.6	12.9	1410	10	US-09-974-760B-87	Sequence 87, Appl
	34	128.6	9.3	1509	17	US-10-149-310-151	Sequence 151, App
	35	128.6	9.3	1512	13	US-10-109-310-27	Sequence 27, Appl
	36	128.6	9.3	33000	13	US-10-109-310-18	Sequence 18, Appl
	37	40	2.9	14859	16	US-10-051-874-55	Sequence 55, Appl
	38	40	2.9	15645	16	US-10-085-198-111	Sequence 111, App
c	39	38.4	2.8	296405	13	US-10-087-192-1036	Sequence 1036, Ap
	40	37.6	2.7	2416	13	US-10-425-114-14168	Sequence 14168, A
c	41	37.4	2.7	671	15	US-10-184-644-346	Sequence 346, App
c	42	37.4	2.7	671	15	US-10-184-634-346	Sequence 346, App
c	43	36.8	2.7	426	13	US-10-085-783A-39856	Sequence 39856, A
c	44	36.8	2.7	426	16	US-10-242-535A-39856	Sequence 39856, A
	45	36.8	2.7	578	13	US-10-425-114-25354	Sequence 25354, A

ALIGNMENTS

RESULT 1
US-09-836-705-41

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 00:41:26 ; Search time 5540 Seconds
(without alignments)
7438.594 Million cell updates/sec

Title: US-09-836-705-41
Perfect score: 1380
Sequence: 1 atgtccctgccgcatgcaac.....agaaacacaatattgcttag 1380

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	43.4	3.1	849	13	BX462111	BX462111 BX462111
c	2	42.8	3.1	712	13	BX416727	BX416727 BX416727
c	3	41.6	3.0	312	12	BI020956	BI020956 IL2-MT017
c	4	40.2	2.9	594	29	CC961677	CC961677 BOIDV75TR
	5	40.2	2.9	724	28	BZ037785	BZ037785 oeh83g04.
	6	40.2	2.9	774	28	BZ440495	BZ440495 BONFF96TF
	7	39.6	2.9	590	28	BZ608116	BZ608116 WHACA05TR
c	8	39.6	2.9	885	13	BX425603	BX425603 BX425603
	9	39.2	2.8	646	12	BM620885	BM620885 170006874
	10	39.2	2.8	666	12	BM609275	BM609275 170006870
	11	39.2	2.8	675	12	BM644593	BM644593 170006873
	12	39.2	2.8	677	12	BM613747	BM613747 170006871
	13	39.2	2.8	681	12	BM593491	BM593491 170006874
	14	39.2	2.8	708	12	BM591948	BM591948 170006874
	15	39.2	2.8	735	12	BM597722	BM597722 170006875
	16	38.6	2.8	676	12	BM625617	BM625617 170006874
	17	38.4	2.8	644	12	BM605179	BM605179 170006870
	18	38.4	2.8	712	28	BH898573	BH898573 MB61p8H7
c	19	38.4	2.8	962	12	BI737623	BI737623 603358532
	20	38.4	2.8	1201	13	BX381961	BX381961 BX381961
c	21	38.2	2.8	353	12	BG986317	BG986317 CM1-HT114
	22	38.2	2.8	473	9	AA843590	AA843590 aj54h09.s
	23	38.2	2.8	549	14	CB014956	CB014956 As_tgz_87
	24	38.2	2.8	574	13	BX492319	BX492319 DKFZp781D
	25	38.2	2.8	965	13	BX359538	BX359538 BX359538
	26	38	2.8	513	14	CA708037	CA708037 wdk2c.pk0
	27	38	2.8	675	13	BY706450	BY706450 BY706450
	28	38	2.8	978	13	BQ929015	BQ929015 AGENCOURT
	29	37.8	2.7	517	12	BM636872	BM636872 170006875
	30	37.8	2.7	645	14	CA727324	CA727324 wde1f.pk0
	31	37.8	2.7	696	12	BM584599	BM584599 170006872
	32	37.6	2.7	621	13	BW265801	BW265801 BW265801
	33	37.6	2.7	658	13	BW265514	BW265514 BW265514
	34	37.6	2.7	663	13	BW259047	BW259047 BW259047
c	35	37.6	2.7	876	29	CG456125	CG456125 PUIJO26TB
	36	37.6	2.7	1933	11	AY325173	AY325173 Rattus no
c	37	37.4	2.7	307	10	BF763590	BF763590 CM1-CS003
	38	37.4	2.7	420	29	CC984990	CC984990 ZUADI29TV
	39	37.4	2.7	426	14	W26494	W26494 30d12 Human
	40	37.4	2.7	440	12	BM278536	BM278536 As_tgz_63
	41	37.4	2.7	446	10	BF755870	BF755870 CM3-CT057
	42	37.4	2.7	586	14	CK093525	CK093525 G123P15.3
	43	37.4	2.7	677	28	AZ573239	AZ573239 315PvB09
	44	37.4	2.7	750	10	BE413590	BE413590 SCU001.A0
	45	37	2.7	530	9	AA961827	AA961827 or61a05.s